

R E M A R K S

Enclosed herewith in full compliance with 37 C.F.R. §§1.821-1.825 is a Substitute Sequence Listing to be inserted into the specification as indicated above. The Substitute Sequence Listing in no way introduces new matter into the specification. Also submitted herewith in full compliance with 37 C.F.R. §§1.821-1.825 is a disk copy of the Substitute Sequence Listing. The disk copy of the Sequence Listing, file "2004-10-11 0760-0329P.ST25.txt", is identical to the paper copy, except that it lacks formatting.

The sequence listing is amended to fix matters of form and to properly identify the present application by filing date and serial number. No new matter is introduced by these amendments.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17; particularly, extension of time fees.

Respectfully submitted,

BIRCH, STEWART, KOLASCH & BIRCH, LLP

By  #42874
Gerald M. Murphy, Jr., #28,977

GMM/CAM:bmp/psq
0760-0329P

P.O. Box 747
Falls Church, VA 22040-0747
(703) 205-8000

Attachments: Disk Copy of Sequence Listing
 Paper Copy of Sequence Listing



SEQUENCE LISTING

<110> Yasuhiko MUNAKATA et al.

<120> NOVEL HUMAN PARVOVIRUS B19 RECEPTOR AND USES THEREOF

<130> 0760-0329P

<140> US 10/768,030

<141> 2004-02-02

<160> 5

<170> PatentIn 3.2

<210> 1

<211> 732

<212> PRT

<213> Homo sapiens

<400> 1

Met	Val	Arg	Ser	Gly	Asn	Lys	Ala	Ala	Val	Val	Leu	Cys	Met	Asp	Val
1				5					10				15		
Gly	Phe	Thr	Met	Ser	Asn	Ser	Ile	Pro	Gly	Ile	Glu	Ser	Pro	Phe	Glu
			20					25				30			
Gln	Ala	Lys	Lys	Val	Ile	Thr	Met	Phe	Val	Gln	Arg	Gln	Val	Phe	Ala
				35				40			45				
Glu	Asn	Lys	Asp	Glu	Ile	Ala	Leu	Val	Leu	Phe	Gly	Thr	Asp	Gly	Thr
			50				55			60					
Asp	Asn	Pro	Leu	Ser	Gly	Gly	Asp	Gln	Tyr	Gln	Asn	Ile	Thr	Val	His
			65				70			75			80		
Arg	His	Leu	Met	Leu	Pro	Asp	Phe	Asp	Leu	Leu	Glu	Asp	Ile	Glu	Ser
				85				90			95				
Lys	Ile	Gln	Pro	Gly	Ser	Gln	Gln	Ala	Asp	Phe	Leu	Asp	Ala	Leu	Ile
			100					105			110				
Val	Ser	Met	Asp	Val	Ile	Gln	His	Glu	Thr	Ile	Gly	Lys	Lys	Phe	Glu
			115					120			125				
Lys	Arg	His	Ile	Glu	Ile	Phe	Thr	Asp	Leu	Ser	Ser	Arg	Phe	Ser	Lys
			130				135			140					
Ser	Gln	Leu	Asp	Ile	Ile	His	Ser	Leu	Lys	Lys	Cys	Asp	Ile	Ser	
			145				150			155			160		
Leu	Gln	Phe	Leu	Pro	Phe	Ser	Leu	Gly	Lys	Glu	Asp	Gly	Ser	Gly	
				165				170			175				
Asp	Arg	Gly	Asp	Gly	Pro	Phe	Arg	Leu	Gly	Gly	His	Gly	Pro	Ser	Phe
			180				185			190					
Pro	Leu	Lys	Gly	Ile	Thr	Glu	Gln	Gln	Lys	Glu	Gly	Leu	Glu	Ile	Val
			195				200			205					
Lys	Met	Val	Met	Ile	Ser	Leu	Glu	Gly	Glu	Asp	Gly	Leu	Asp	Glu	Ile
			210				215			220					
Tyr	Ser	Phe	Ser	Glu	Ser	Leu	Arg	Lys	Leu	Cys	Val	Phe	Lys	Lys	Ile
			225				230			235			240		
Glu	Arg	His	Ser	Ile	His	Trp	Pro	Cys	Arg	Leu	Thr	Ile	Gly	Ser	Asn
				245				250			255				
Leu	Ser	Ile	Arg	Ile	Ala	Ala	Tyr	Lys	Ser	Ile	Leu	Gln	Glu	Arg	Val
			260				265			270					
Lys	Lys	Thr	Trp	Thr	Val	Val	Asp	Ala	Lys	Thr	Leu	Lys	Lys	Glu	Asp
			275				280			285					

Ile Gln Lys Glu Thr Val Tyr Cys Leu Asn Asp Asp Asp Glu Thr Glu
 290 295 300
 Val Leu Lys Glu Asp Ile Ile Gln Gly Phe Arg Tyr Gly Ser Asp Ile
 305 310 315 320
 Val Pro Phe Ser Lys Val Asp Glu Glu Gln Met Lys Tyr Lys Ser Glu
 325 330 335
 Gly Lys Cys Phe Ser Val Leu Gly Phe Cys Lys Ser Ser Gln Val Gln
 340 345 350
 Arg Arg Phe Phe Met Gly Asn Gln Val Leu Lys Val Phe Ala Ala Arg
 355 360 365
 Asp Asp Glu Ala Ala Ala Val Ala Leu Ser Ser Leu Ile His Ala Leu
 370 375 380
 Asp Asp Leu Asp Met Val Ala Ile Val Arg Tyr Ala Tyr Asp Lys Arg
 385 390 395 400
 Ala Asn Pro Gln Val Gly Val Ala Phe Pro His Ile Lys His Asn Tyr
 405 410 415
 Glu Cys Leu Val Tyr Val Gln Leu Pro Phe Met Glu Asp Leu Arg Gln
 420 425 430
 Tyr Met Phe Ser Ser Leu Lys Asn Ser Lys Lys Tyr Ala Pro Thr Glu
 435 440 445
 Ala Gln Leu Asn Ala Val Asp Ala Leu Ile Asp Ser Met Ser Leu Ala
 450 455 460
 Lys Lys Asp Glu Lys Thr Asp Thr Leu Glu Asp Leu Phe Pro Thr Thr
 465 470 475 480
 Lys Ile Pro Asn Pro Arg Phe Gln Arg Leu Phe Gln Cys Leu Leu His
 485 490 495
 Arg Ala Leu His Pro Arg Glu Pro Leu Pro Pro Ile Gln Gln His Ile
 500 505 510
 Trp Asn Met Leu Asn Pro Pro Ala Glu Val Thr Thr Lys Ser Gln Ile
 515 520 525
 Pro Leu Ser Lys Ile Lys Thr Leu Phe Pro Leu Ile Glu Ala Lys Lys
 530 535 540
 Lys Asp Gln Val Thr Ala Gln Glu Ile Phe Gln Asp Asn His Glu Asp
 545 550 555 560
 Gly Pro Thr Ala Lys Lys Leu Lys Thr Glu Gln Gly Gly Ala His Phe
 565 570 575
 Ser Val Ser Ser Leu Ala Glu Gly Ser Val Thr Ser Val Gly Ser Val
 580 585 590
 Asn Pro Ala Glu Asn Phe Arg Val Leu Val Lys Gln Lys Lys Ala Ser
 595 600 605
 Phe Glu Glu Ala Ser Asn Gln Leu Ile Asn His Ile Glu Gln Phe Leu
 610 615 620
 Asp Thr Asn Glu Thr Pro Tyr Phe Met Lys Ser Ile Asp Cys Ile Arg
 625 630 635 640
 Ala Phe Arg Glu Glu Ala Ile Lys Phe Ser Glu Glu Gln Arg Phe Asn
 645 650 655
 Asn Phe Leu Lys Ala Leu Gln Glu Lys Val Glu Ile Lys Gln Leu Asn
 660 665 670
 His Phe Trp Glu Ile Val Val Gln Asp Gly Ile Thr Leu Ile Thr Lys
 675 680 685
 Glu Glu Ala Ser Gly Ser Ser Val Thr Ala Glu Glu Ala Lys Lys Phe
 690 695 700
 Leu Ala Pro Lys Asp Lys Pro Ser Gly Asp Thr Ala Ala Val Phe Glu
 705 710 715 720
 Glu Gly Gly Asp Val Asp Asp Leu Leu Asp Met Ile
 725 730

aaa gaa ggt ctt gag ata gtg aaa atg gtg atg ata tct tta gaa ggt Lys Glu Gly Leu Glu Ile Val Lys Met Val Met Ile Ser Leu Glu Gly 205 210 215	678
gaa gat ggg ttg gat gaa att tat tca ttc agt gag agt ctg aga aaa Glu Asp Gly Leu Asp Glu Ile Tyr Ser Phe Ser Glu Ser Leu Arg Lys 220 225 230	726
ctg tgc gtc ttc aag aaa att gag agg cat tcc att cac tgg ccc tgc Leu Cys Val Phe Lys Lys Ile Glu Arg His Ser Ile His Trp Pro Cys 235 240 245	774
cga ctg acc att ggc tcc aat ttg tct ata agg att gca gcc tat aaa Arg Leu Thr Ile Gly Ser Asn Leu Ser Ile Arg Ile Ala Ala Tyr Lys 250. 255 260 265	822
tcg att cta cag gag aga gtt aaa aag act tgg aca gtt gtg gat gca Ser Ile Leu Gln Glu Arg Val Lys Lys Thr Trp Thr Val Val Asp Ala 270 275 280	870
aaa acc cta aaa aaa gaa gat ata caa aaa gaa aca gtt tat tgc tta Lys Thr Leu Lys Lys Glu Asp Ile Gln Lys Glu Thr Val Tyr Cys Leu 285 290 295	918
aat gat gat gat gaa act gaa gtt tta aaa gag gat att att caa ggg Asn Asp Asp Asp Glu Thr Glu Val Leu Lys Glu Asp Ile Ile Gln Gly 300 305 310	966
ttc cgc tat gga agt gat ata gtt cct ttc tct aaa gtg gat gag gaa Phe Arg Tyr Gly Ser Asp Ile Val Pro Phe Ser Lys Val Asp Glu Glu 315 320 325	1014
caa atg aaa tat aaa tcg gag ggg aag tgc ttc tct gtt ttg gga ttt Gln Met Lys Tyr Lys Ser Glu Gly Lys Cys Phe Ser Val Leu Gly Phe 330 335 340 345	1062
tgt aaa tct tct cag gtt cag aga aga ttc ttc atg gga aat caa gtt Cys Lys Ser Ser Gln Val Gln Arg Arg Phe Phe Met Gly Asn Gln Val 350 355 360	1110
cta aag gtc ttt gca gca aga gat gat gag gca gct gca gtt gca ctt Leu Lys Val Phe Ala Ala Arg Asp Asp Glu Ala Ala Ala Val Ala Leu 365 370 375	1158
tcc tcc ctg att cat gct ttg gat gac tta gac atg gtg gcc ata gtt Ser Ser Leu Ile His Ala Leu Asp Asp Leu Asp Met Val Ala Ile Val 380 385 390	1206
cga tat gct tat gac aaa aga gct aat cct caa gtc ggc gtg gct ttt Arg Tyr Ala Tyr Asp Lys Arg Ala Asn Pro Gln Val Gly Val Ala Phe 395 400 405	1254
cct cat atc aag cat aac tat gag tgt tta gtg tat gtg cag ctg cct Pro His Ile Lys His Asn Tyr Glu Cys Leu Val Tyr Val Gln Leu Pro 410 415 420 425	1302

ttc atg gaa gac ttg cg ^g caa tac atg ttt tca tcc ttg aaa aac agt Phe Met Glu Asp Leu Arg Gln Tyr Met Phe Ser Ser Leu Lys Asn Ser 430 435 440	1350
aag aaa tat gct ccc acc gag gca cag ttg aat gct gtt gat gct ttg Lys Lys Tyr Ala Pro Thr Glu Ala Gln Leu Asn Ala Val Asp Ala Leu 445 450 455	1398
att gac tcc atg agc ttg gca aag aaa gat gag aag aca gac acc ctt Ile Asp Ser Met Ser Leu Ala Lys Lys Asp Glu Lys Thr Asp Thr Leu 460 465 470	1446
gaa gac ttg ttt cca acc acc aaa atc cca aat cct cga ttt cag aga Glu Asp Leu Phe Pro Thr Thr Lys Ile Pro Asn Pro Arg Phe Gln Arg 475 480 485	1494
tta ttt cag tgt ctg ctg cac aga gct tta cat ccc cgg gag cct cta Leu Phe Gln Cys Leu Leu His Arg Ala Leu His Pro Arg Glu Pro Leu 490 495 500 505	1542
ccc cca att cag cag cat att tgg aat atg ctg aat cct ccc gct gag Pro Pro Ile Gln Gln His Ile Trp Asn Met Leu Asn Pro Pro Ala Glu 510 515 520	1590
gtg aca aca aaa agt cag att cct ctc tct aaa ata aag acc ctt ttt Val Thr Thr Lys Ser Gln Ile Pro Leu Ser Lys Ile Lys Thr Leu Phe 525 530 535	1638
cct ctg att gaa gcc aag aaa aag gat caa gtg act gct cag gaa att Pro Leu Ile Glu Ala Lys Lys Asp Gln Val Thr Ala Gln Glu Ile 540 545 550	1686
ttc caa gac aac cat gaa gat gga cct aca gct aaa aaa tta aag act Phe Gln Asp Asn His Glu Asp Gly Pro Thr Ala Lys Lys Leu Lys Thr 555 560 565	1734
gag caa ggg gga gcc cac ttc agc gtc tcc agt ctg gct gaa ggc agt Glu Gln Gly Gly Ala His Phe Ser Val Ser Ser Leu Ala Glu Gly Ser 570 575 580 585	1782
gtc acc tct gtt gga agt gtg aat cct gct gaa aac ttc cgt gtt cta Val Thr Ser Val Gly Ser Val Asn Pro Ala Glu Asn Phe Arg Val Leu 590 595 600	1830
gtg aaa cag aag aag gcc agc ttt gag gaa gcg agt aac cag ctc ata Val Lys Gln Lys Lys Ala Ser Phe Glu Glu Ala Ser Asn Gln Leu Ile 605 610 615	1878
aat cac atc gaa cag ttt ttg gat act aat gaa aca ccg tat ttt atg Asn His Ile Glu Gln Phe Leu Asp Thr Asn Glu Thr Pro Tyr Phe Met 620 625 630	1926
aag agc ata gac tgc atc cga gcc ttc cgg gaa gaa gcc att aag ttt Lys Ser Ile Asp Cys Ile Arg Ala Phe Arg Glu Glu Ala Ile Lys Phe 635 640 645	1974
tca gaa gag cag cgc ttt aac aac ttc ctg aaa gcc ctt caa gag aaa	2022

Ser	Glu	Glu	Gln	Arg	Phe	Asn	Asn	Phe	Leu	Lys	Ala	Leu	Gln	Glu	Lys	
650					655				660					665		
gtg	gaa	att	aaa	caa	tta	aat	cat	ttc	tgg	gaa	att	gtt	gtc	cag	gat	2070
Val	Glu	Ile	Lys	Gln	Leu	Asn	His	Phe	Trp	Glu	Ile	Val	Val	Gln	Asp	
					670				675					680		
gga	att	act	ctg	atc	acc	aaa	gag	gaa	gcc	tct	gga	agt	tct	gtc	aca	2118
Gly	Ile	Thr	Leu	Ile	Thr	Lys	Glu	Glu	Ala	Ser	Gly	Ser	Ser	Val	Thr	
					685				690					695		
gct	gag	gaa	gcc	aaa	aag	ttt	ctg	gcc	ccc	aaa	gac	aaa	cca	agt	gga	2166
Ala	Glu	Glu	Ala	Lys	Lys	Phe	Leu	Ala	Pro	Lys	Asp	Lys	Pro	Ser	Gly	
					700				705					710		
gac	aca	gca	gct	gta	ttt	gaa	gaa	ggt	ggt	gat	gtg	gac	gat	tta	ttg	2214
Asp	Thr	Ala	Ala	Val	Phe	Glu	Glu	Gly	Gly	Asp	Val	Asp	Asp	Leu	Leu	
					715				720					725		
gac	atg	ata	tag	gtcgtggatg	tatggggat	ctaagagagc	tgccatcgct									2266
Asp	Met	Ile														
	730															
gtgatgctgg	gagttctaac	aaaacaagg	tttgcggcc	attcaagggg	agccaaaatc											2326
tcaagaaatt	cccacaggt	tacctggagg	cgatcatct	aattctctgt	ggaatgaata											2386
cacacatata	tattacaagg	gataatttag	accccataca	agtttataaa	gagtcattgt											2446
tatTTTCTGG	ttgggtgtatt	atTTTTCTG	ttggttact	gatctttgt	tattacatac											2506
atgctttgaa	gtttctggaa	agtagatctt	ttcttgacct	agtatatcag	tgacagttgc											2566
agcccttgc	atgtgattag	tgtctcatgt	ggaaccatgg	catggttatt	gatgagttc											2626
ttaaccctt	ccagagtcct	ccttgcctg	atcctccaac	agctgtcaca	acttgtgtt											2686
agaaggcagt	agcatttgct	tcctccaaac	aagcagctgg	gttaggaaa	ccatggtaa											2746
ggacggactc	acttctttt	ttagttgagg	ccttctagtt	accacattac	tctgcctctg											2806
tatatagg	gttttctta	agtgggggtgg	gaaggggagc	acaatttccc	ttcataactcc											2866
ttttaagcag	tgagttatgg	tgtgtgtctc	atgaagaaaa	gaccttttgg	cccaatctct											2926
gccatatcag	tgaaccttta	gaaactcaaa	aactgagaaa	tttacttcag	tagttagaat											2986
tatatacatt	cactgttctc	tacttgcaag	cctcaaagag	agaaaagtttc	gttatattaa											3046
aacactttagg	taacttttcg	gtctttccca	tttctaccta	agtcagctt	catctttgt											3106
gatgggtgtct	ccttactaa	ataagaaaat	aacaaagccc	ttattcttt	tttttctt											3166
cctcattctt	gccttgagtt	coagttcctc	tttgggtgtac	agacttctt	gtacccagtc											3226
acctctgtct	tcagcacccct	cataagtcgt	cactaataca	cagttttgt	catgtaacat											3286
taaaggcata	aatgactc															3304

<210> 3
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer for real-time detection PCR

<400> 3
ccctagaaaa cccatcctct gtg

<210> 4
<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer for real-time detection PCR

<400> 4
aggttctgca tgactgctac tgg 23

<210> 5
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide probe for real-time detection PCR

<400> 5
tcatggacag ttatctgacc accccca 27